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(1) GENERAL INFORMATION:

(i) APPLICANT: Bujard, Hermann
Gossen, Manfred

(ii) TITLE OF INVENTION: Animals Transgenic for a Tetracycline-Inducible Transcriptional Activator

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/383,754
(B) FILING DATE: 03-FEB-1995
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/275,876
(B) FILING DATE: 15-JULY-94
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/270,637
(B) FILING DATE: 01-JULY-94
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/260,452
(B) FILING DATE: 14-JUNE-94
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/076,327
(B) FILING DATE: 14-JUNE-93
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: US 08/076,726

(B) FILING DATE: 14-JUNE-93

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: DeConti, Giulio A. Jr.

(B) REGISTRATION NUMBER: 31,503

(C) REFERENCE/DOCKET NUMBER: BBI-009CP3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400

(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1008 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 1..1008

(ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 1..1008

(ix) FEATURE:

(A) NAME/KEY: misc. binding

(B) LOCATION: 1..207

(ix) FEATURE:

(A) NAME/KEY: misc. binding

(B) LOCATION: 208..335

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG 48
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG 96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG 144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

	CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT	192
	Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
	50 55 60	
5	ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC	240
	Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg	
	65 70 75 80	
10	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA	288
	Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly	
	85 90 95	
15	GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT	336
	Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
	100 105 110	
20	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG	384
	Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
	115 120 125	
	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432
	Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
	130 135 140	
25	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480
	Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
	145 150 155 160	
30	CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA	528
	Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	
	165 170 175	
35	TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG	576
	Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	
	180 185 190	
40	ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG	624
	Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala	
	195 200 205	
	TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC	672
	Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly	
	210 215 220	
45	CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG	720
	Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala	
	225 230 235 240	
50	GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG	768
	Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser	
	245 250 255	
55	ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC	816
	Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp	
	260 265 270	
	GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT	864
	Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp	
	275 280 285	

CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC 912
 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
 290 295 300

CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT 960
 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
 305 310 315 320

GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG 1008
 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
 325 330 335

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15

Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45

Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50 55 60

Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80

Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
 85 90 95

Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
 115 120 125

Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
 130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
 145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
 165 170 175

Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
 180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
195 200 205

5 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
210 215 220

10 Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
225 230 235 240

Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
245 250 255

15 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
260 265 270

Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
275 280 285

20 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
290 295 300

25 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
305 310 315 320

Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
325 330 335

30 INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG 33
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
1 5 10

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 Met Pro Lys Arg Pro Arg Pro
1 5

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG	60
TGGATGGCGT CTCCAGGCGA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA	120
45 GTTTACCACT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA	180
GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA	240
50 AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC	300
CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA	360
AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG	420
55 TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA	480
ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTTGA CCTCCATAGA AGACACCGGG	540

ACCGATCCAG CCTCCGCGGC CCCGAATTC

569

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 520 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGATCTGCAG GGTCTGCTCGG TGTTCGAGGC CACACGCGTC ACCTTAATAT GCGAAGTGGG 60
CCGGATCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 120
ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 180
AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 240
TTTACCACTC CCTATCAGTG ATAGAGAAAA GTGAAAGTCG AGTTTACCAC TCCCTATCAG 300
TGATAGAGAA AAGTGAAAGT CGAGTTTACC ACTCCCTATC AGTGATAGAG AAAAGTGAAA 360
GTCGAGCTCG GTACCCGGGT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 420
TCGTTTGTAGT AACCCTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTGT ACCTCCATAG 480
AAGACACCGG GACCGATCCA GCCTCCGCGG CCCGAATTC 520

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Human cytomegalovirus
(B) STRAIN: K12, Towne

- (ix) FEATURE:
(A) NAME/KEY: mRNA
(B) LOCATION: 382..450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC 60
ACTCCCTATC AGTGATAGAG AAAAGTGAAA GTCGAGTTTA CCACTCCCTA TCAGTGATAG 120

AGAAAAGTGA AAGTCGAGTT TACCACTCCC TATCAGTGAT AGAGAAAAGT GAAAGTCGAG 180
TTTACCACTC CCTATCAGTG ATAGAGAAAA GTGAAAGTCG AGTTTACCAC TCCCTATCAG 240
TGATAGAGAA AAGTGAAAGT CGAGTTTACC ACTCCCTATC AGTGATAGAG AAAAGTGAAA 300
GTCGAGCTCG GTACCCGGGT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 360
5 TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG 420
AAGACACCGG GACCGATCCA GCCTCCGCGG 450

(2) INFORMATION FOR SEQ ID NO:9:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Human cytomegalovirus
20 (B) STRAIN: Towne
- (ix) FEATURE:
(A) NAME/KEY: mRNA
(B) LOCATION: 382..450

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCTCG ACCCGGGTAC CGAGCTCGAC TTTCACTTTT CTCTATCACT GATAGGGAGT 60
GGTAAACTCG ACTTTCACTT TTCTCTATCA CTGATAGGGA GTGGTAAACT CGACTTTCAC 120
TTTTCTCTAT CACTGATAGG GAGTGGTAAA CTCGACTTTC ACTTTTCTCT ATCACTGATA 180
GGGAGTGGTA AACTCGACTT TCACTTTTCT CTATCACTGA TAGGGAGTGG TAAACTCGAC 240
30 TTTCACTTTT CTCTATCACT GATAGGGAGT GGTAAACTCG ACTTTCACTT TTCTCTATCA 300
CTGATAGGGA GTGGTAAACT CGAGTAGGCG TGTACGGTGG GAGGCCTATA TAAGCAGAGC 360
TCGTTTAGTG AACCGTCAGA TCGCCTGGAG ACGCCATCCA CGCTGTTTTG ACCTCCATAG 420
AAGACACCGG GACCGATCCA GCCTCCGCGG 450

35 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Herpes Simplex Virus
(B) STRAIN: KOS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5 GAGCTCGACT TTCACTTTTC TCTATCACTG ATAGGGAGTG GTAAACTCGA CTTTCACTTT 60
10 TCTCTATCAC TGATAGGGAG TGGTAAACTC GACTTTCACT TTTCTCTATC ACTGATAGGG 120
AGTGGTAAAC TCGACTTTCA CTTTCTCTA TCACTGATAG GGAGTGGTAA ACTCGACTTT 180
CACTTTTCTC TATCACTGAT AGGGAGTGGT AACTCGACT TTCACTTTTC TCTATCACTG 240
ATAGGGAGTG GTAAACTCGA CTTTCACTTT TCTCTATCAC TGATAGGGAG TGGTAAACTC 300
GAGATCCGGC GAATTCGAAC ACGCAGATGC AGTCGGGGCG GCGCGGTCCG AGGTCCACTT 360
15 CGCATATTAA GGTGACGCGT GTGGCCTCGA ACACCGAG 398

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTTTATCAC TGATAAACAA ACTTATCAGT GATAAAGA 38

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACTCTATCAT TGATAGAGTT CCCTATCAGT GATAGAGA 38

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTATCAT CGATAAGCTA GTTTATCACA GTTAAATT

38

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCTATCAT TGATAGGGAA CTCTATCAAT GATAGGGA

38

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATCTATCAC TGATAGAGTA CCCTATCATC GATAGAGA

38

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG	48
	Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu	
	1 5 10 15	
10	CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG	96
	Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
	20 25 30	
15	AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG	144
	Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
	35 40 45	
20	CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT	192
	Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
	50 55 60	
25	ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT	240
	Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg	
	65 70 75 80	
30	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA	288
	Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly	
	85 90 95	
35	GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT	336
	Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
	100 105 110	
40	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG	384
	Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
	115 120 125	
45	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432
	Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
	130 135 140	
50	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480
	Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
	145 150 155 160	
55	CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA	528
	Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	
	165 170 175	
60	TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG	576
	Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	
	180 185 190	
65	ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC	621
	Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser	
	195 200 205	

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1             5             10             15
10 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
    20             25             30
    Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
    35             40             45
15 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
    50             55             60
    Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
    65             70             75             80
    Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
    85             90             95
25 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
    100            105            110
    Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
    115            120            125
30 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
    130            135            140
    Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
    145            150            155            160
    Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
    165            170            175
40 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
    180            185            190
    Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
    195            200            205
45

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

F01090" 00000000

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

5	ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG	48
	Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu	
	1 5 10 15	
10	CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG	96
	Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln	
	20 25 30	
15	AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG	144
	Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys	
	35 40 45	
	CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT	192
	Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His	
	50 55 60	
20	ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC	240
	Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg	
	65 70 75 80	
25	AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA	288
	Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly	
	85 90 95	
30	GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT	336
	Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr	
	100 105 110	
35	CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG	384
	Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu	
	115 120 125	
	AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC	432
	Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys	
	130 135 140	
40	GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA	480
	Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr	
	145 150 155 160	
45	CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA	528
	Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu	
	165 170 175	
50	TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG	576
	Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu	
	180 185 190	
55	ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC	621
	Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser	
	195 200 205	

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
1 5 10 15

10 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
20 25 30

Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
35 40 45

15 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
50 55 60

20 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
65 70 75 80

Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
85 90 95

25 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
100 105 110

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125

30 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
130 135 140

Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145 150 155 160

Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
165 170 175

40 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
180 185 190

Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
195 200 205

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

	CTG GAC GAC TCG AAG CGC GTA GCC AAG CGG AAG CTG ATC GAG GAG AAC	48
	Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn	
	1 5 10 15	
5	CGG GAG CGG CGA CGC AAG GAG GAG ATG ATC AAA TCC CTG CAG CAC CGG	96
	Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg	
	20 25 30	
10	CCC AGC CCC AGC GCA GAG GAG TGG GAG CTG ATC CAC GTG GTG ACC GAG	144
	Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu	
	35 40 45	
15	GCG CAC CGC AGC ACC AAC GCG CAG GGC AGC CAC TGG AAG CAG AGG AGG	192
	Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg	
	50 55 60	
20	AAA TTC CTG CTC GAA GAT ATC GGT CAG TCG CCC ATG GCC TCC ATG CTT	240
	Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu	
	65 70 75 80	
25	GAC GGG GAC AAA GTG GAC CTG GAG GCG TTC AGC GAG TTT ACA AAA ATC	288
	Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile	
	85 90 95	
30	ATC ACG CCG GCC ATC ACC CGC GTG GTC GAC TTT GCC AAA AAC CTG CCC	336
	Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro	
	100 105 110	
35	ATG TTC TCG GAG CTG CCG TGC GAG GAT CAG ATC ATC CTG CTG AAG GGC	384
	Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly	
	115 120 125	
40	TGC TGC ATG GAG ATC ATG TCG CTG CGC GCC GCC GTG CGC TAC GAC CCC	432
	Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro	
	130 135 140	
45	GAG AGC GAA ACG CTG ACG CTG AGC GGG GAA ATG GCC GTC AAA CGC GAG	480
	Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu	
	145 150 155 160	
50	CAG TTG AAG AAC GGA GGG CTG GGG GTC GTG TCT GAT GCC ATC TTC GAC	528
	Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp	
	165 170 175	
55	CTC GGC AAG TCG CTG TCT GCC TTC AAC CTG GAC GAC ACC GAG GTG GCC	576
	Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala	
	180 185 190	
60	CTG CTG CAG GCC GTG CTG CTC ATG TCC TCA GAC CGG ACG GGG CTG ATC	624
	Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile	
	195 200 205	
65	TGC GTG GAT AAG ATA GAG AAG TGC CAG GAG TCG TAC CTG CTG GCG TTC	672
	Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe	
	210 215 220	
70	GAG CAC TAC ATC AAC TAC CGC AAA CAC AAC ATT CCC CAC TTC TGG TCC	720
	Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser	
	225 230 235 240	

AAG CTG CTG ATG AAG GTG GCG GAC CTG CGC ATG ATC GGC GCC TAC CAC 768
Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His
245 250 255

GCC AGC CGC TTC CTG CAC ATG AAG GTG GAG TGC CCC ACC GAG CTC TCC 816
Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser
260 265 270

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

20 Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn
1 5 10 15
Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg
20 25 30
25 Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu
35 40 45
30 Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg
50 55 60
Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu
65 70 75 80
35 Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile
85 90 95
Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro
100 105 110
40 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly
115 120 125
Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro
130 135 140
45 Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu
145 150 155 160
50 Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp
165 170 175
Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala
180 185 190
55 Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile

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Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe
210 215 220

Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser
225 230 235 240

Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His
245 250 255

Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser
260 265 270

15 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCCCCGGGTA ACTAAGTAAG GATCC

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(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTGGGTCCC CGGGTGACAT GGAA

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(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

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